



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/666,806

Source:

IPW

Date Processed by STIC:

3/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS.

<http://www.uspto.gov/web/offices/pat/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

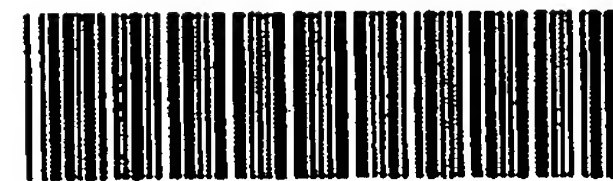
SERIAL NUMBER:

10/666, 806

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/666,806

DATE: 03/24/2004
TIME: 15:09:10

Input Set : A:\4798 Seq List.ST25.txt
Output Set: N:\CRF4\03242004\J666806.raw

3 <110> APPLICANT: Aydin, Atakan
5 <120> TITLE OF INVENTION: Methods and Compositions for Detecting Targets
7 <130> FILE REFERENCE: 4798US
9 <140> CURRENT APPLICATION NUMBER: US 10/666,806
10 <141> CURRENT FILING DATE: 2003-09-19
12 <150> PRIOR APPLICATION NUMBER: US 60/412,189
13 <151> PRIOR FILING DATE: 2002-09-19
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 49
21 <212> TYPE: DNA
C--> 22 <213> ORGANISM: Homo sapiens and Artificial
W--> 24 <220> FEATURE:
W--> 24 <223> OTHER INFORMATION: -IF <213> Response is Artificial/
W--> 24 <400> 1 Unknown, please explain in section <220> - <223>
25 ttgcctgctc gacttagatc aaaggagacg cggctgcttt cagcctcat
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 49
30 <212> TYPE: DNA
C--> 31 <213> ORGANISM: Homo sapiens and Artificial
W--> 33 <220> FEATURE:
W--> 33 <223> OTHER INFORMATION:
W--> 33 <400> 2
34 ttgcctgctc gacttagagg gtcacagtag gtggtgcttt cagcctcac
37 <210> SEQ ID NO: 3
38 <211> LENGTH: 33
39 <212> TYPE: DNA
C--> 40 <213> ORGANISM: Homo sapiens and Artificial
W--> 42 <220> FEATURE:
W--> 42 <223> OTHER INFORMATION:
W--> 42 <400> 3
43 ggggatagtg gctgcatcac tggatagcga cgt
46 <210> SEQ ID NO: 4
47 <211> LENGTH: 49
48 <212> TYPE: DNA
C--> 49 <213> ORGANISM: Homo sapiens and Artificial
W--> 51 <220> FEATURE:
W--> 51 <223> OTHER INFORMATION:
W--> 51 <400> 4
52 ttgcctgctc gacttagatc aaaggagacg cggcagtggg ttccaacg
55 <210> SEQ ID NO: 5
56 <211> LENGTH: 51

Handwritten notes:
Mandatory, <213> Response has to be either Artificial/Unknown
Does Not Comply Corrected Diskette Needed OR (pg. 16)
Genus Species.
Please see item #10 on error summary sheet.
SAME error
Also pls see error explanation on page 3.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/666,806

DATE: 03/24/2004

TIME: 15:09:10

Input Set : A:\4798 Seq List.ST25.txt

Output Set: N:\CRF4\03242004\J666806.raw

```

57 <212> TYPE: DNA
C--> 58 <213> ORGANISM: Homo sapiens and Artificial - same error
W--> 60 <220> FEATURE:
W--> 60 <223> OTHER INFORMATION:
W--> 60 <400> 5
61 ttgcctgctc gacttagagg gtcacagtag gtggacagtg gttttccaac a 51
64 <210> SEQ ID NO: 6
65 <211> LENGTH: 32
66 <212> TYPE: DNA
C--> 67 <213> ORGANISM: Homo sapiens and Artificial - same error
W--> 69 <220> FEATURE:
W--> 69 <223> OTHER INFORMATION:
W--> 69 <400> 6
70 tgaacacacc gggatatcact ggatagcgac gt 32
73 <210> SEQ ID NO: 7
74 <211> LENGTH: 18
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Synthetic DNA
81 <400> SEQUENCE: 7
82 ttgcctgctc gacttaga 18
85 <210> SEQ ID NO: 8
86 <211> LENGTH: 18
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Synthetic DNA
93 <400> SEQUENCE: 8
94 acgtcgctat ccagtgat 18
97 <210> SEQ ID NO: 9
98 <211> LENGTH: 15
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 9
103 ccgcgtctcc tttga 15
106 <210> SEQ ID NO: 10
107 <211> LENGTH: 16
108 <212> TYPE: DNA
109 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 10
112 ccacctactg tgaccc 16

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/666,806

DATE: 03/24/2004
TIME: 15:09:11

Input Set : A:\4798 Seq List.ST25.txt
Output Set: N:\CRF4\03242004\J666806.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6

ERROR EXPLANATION: 2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/666,806

DATE: 03/24/2004

TIME: 15:09:11

Input Set : A:\4798 Seq List.ST25.txt

Output Set: N:\CRF4\03242004\J666806.raw

L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:24 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:24 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24
L:31 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:33 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:33 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:33
L:40 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:42 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:42 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:42
L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:51 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:51 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:51
L:58 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:60 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:60 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:60 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:60
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:69 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:69 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:69